#8

PCT09

RAW SEQUENCE LISTING DATE: 08/14/2001
PATENT APPLICATION: US/09/890,782 TIME: 10:55:50

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08142001\I890782.raw

ENTERED

<110> APPLICANT: Rijksuniversiteit Leiden

<120> TITLE OF INVENTION: method of modulating metabolite biosynthesis in recombinant cells

<130> FILE REFERENCE: BO 43339

<140> CURRENT APPLICATION NUMBER: US/09/890,782

<141> CURRENT FILING DATE: 2001-08-06

<160> NUMBER OF SEQ ID NOS: 21

<170> SOFTWARE: PatentIn Ver. 2.1

<210> SEQ ID NO: 1

<211> LENGTH: 1754

<212> TYPE: DNA

<213> ORGANISM: Catharanthus roseus

<400> SEQUENCE: 1

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ttcgtttttg taaagtttga ttcttggcgg agattttcga caaaggagtg ggcaatttgt 180
gcaatacttc tgagaaaatt gaaagagata caaggatggc tcttcttgat caggcatcca 240
atttgagtcc catgcctttt gatttcacta gaaagaggaa gtcgaggagg agggatggta 300
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tagatggagg gaaaccagct cggaaggttc ctgccaaagg atcaaaaaag ggatgtatga 420
aaggtaaagg aggccctgag aattctcact gcaaatacag aggagttagg cagaggacat 480
ggggtaaatg ggtggccgaa attcgggaac caaacagggg tagcaggctt tggttgggta 540
cattcagaaa cgcgatagaa gctgcacttg cttatgatga agcagcgagg gcgatgtatg 600
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caacaacatc aggatcagat acgactactg cttctggcat ctcagaggtc tctgtctatg 720
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<210> SEQ ID NO: 2

<211> LENGTH: 885

<212> TYPE: DNA

<213> ORGANISM: Catharanthus roseus

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60 <400> SEQUENCE: 2
61 caacaataat gtatcaatca aatgcccata attccgatca tctaaccttc ttaccacctt 60
62 tagtagatta tcaattcctc aacaacgatt ttgatttttc agaaatattt acagatttca 120
63 attacgctaa ttataattat aatacttcta cctcagataa tttctctggt tttcaattca 180
64 atgaaaattg cgaagaaatt atttcaccaa attatgcttc ggaagattta tcggatatta 240
65 ttttaacaga tattttcaag gatcaggata attacgaaga cgaagtcgtt gcgggagaac 300
66 aagaagaaga attaattacg acacctacct ctcgcggcgg cggcggcggc ggatgtgagc 360
67 agagatcgaa tgaggaatgg attaggtacc gtggcgttag acggcggcca tgggggaaat 420
68 tcgctgcgga aatcagggat cccaagagaa aaggatcgag gatatggttg ggaacttacg 480
69 agacggcgga agatgcggca ttagctttcg atcaagcggc gtttcaactc cgtggttcta 540
70 gagctaggtt aaattttccc aatcttattg gttctgctaa tgctccggtt agagtaagtc 600
71 ctagacgccg atcttcatcg tgtcatcttc gtcctcaata atcctatcca cagttccatg 660
72 gggatagtaa atttttttctt tgagtttttt agaagttata ttatctattg aaaaaataca 720
73 aaacattgca aatatttttt tagtacgtct ctatacttct ttttagtaat attcggatca 780
74 tgagcatggg gaaggtgata ttatccattg tcataaatta atagatacag tatcataaat 840
75 taatatgtac gaattacaag taaaatatag taagtgttaa tattg 885
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79 <211> LENGTH: 792
80 <212> TYPE: DNA
81 <213> ORGANISM: Catharanthus roseus
83 <400> SEQUENCE: 3
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85 tccttaatcg aagaacatct tctcagcgat aattctgatg attccagctc ggaattgact 120
86 tctacagagg aaaattggga agaaattttt gcagattttc taaattggtc gggatccgaa 180
87 atacagaaac gcggtagccc gagttccgaa agctgtcaat cgaattcaat ggcggaaagc 240
88 tgtcaggagg attctgttgt gggaaccccg ccagaagcgg cggccggagg aggttgttcg 300
89 aaggattgga accggtataa gggcgttaga cggcggccgt gggggaagtt cgcggcggag 360
90 ataagggatc cgaaaaagaa aggatccagg atttggttgg gtacatacga gacacctgag 420
91 gatgcagcat tggcttatga tgcagccgcg tttaatatgc gtggagctaa agctaggctt 480
92 aattttcctc atttgattgg ttcgaatatt tccggacccg ttagagtaaa cccgagaaaa 540
93 cgtttccctg cggagccttc tacgacgtcg tcgtcttctt cttcttcttc gtctgaaaat 600
94 agtggaggaa ggaagaagag acgatattaa ttaattatta aaagtggagg attaaaaaaa 660
95 ttctgtgaaa tgagagatta ttacgtggtt tttgttaagc ccgataatcc ctcattgtaa 720
96 aattattaac ttcatcgatg ttctttttta aatctttgga atgtacaaaa ttttatatcc 780
97 aaaaaagttc ac 792
100 <210> SEQ ID NO: 4
101 <211> LENGTH: 376
102 <212> TYPE: PRT
103 <213> ORGANISM: Catharanthus roseus
105 <400> SEQUENCE: 4
106 Met Ala Leu Leu Asp Gln Ala Ser Asn Leu Ser Pro Met Pro Phe Asp
107 1 5 10 15
109 Phe Thr Arg Lys Arg Lys Ser Arg Arg Arg Asp Gly Thr Lys Asn Val
110 20 25 30
112 Ala Glu Thr Leu Ala Lys Trp Lys Glu Tyr Asn Glu Lys Leu Asp Ala
113 35 40 45
115 Leu Asp Gly Gly Lys Pro Ala Arg Lys Val Pro Ala Lys Gly Ser Lys
116 50 55 60
118 Lys Gly Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser His Cys Lys

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119  65                  70                  75                  80
121 Tyr Arg Gly Val Arg Gln Arg Thr Trp Gly Lys Trp Val Ala Glu Ile
122                  85                  90                  95
124 Arg Glu Pro Asn Arg Gly Ser Arg Leu Trp Leu Gly Thr Phe Arg Asn
125             100                 105                 110
127 Ala Ile Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ala Arg Ala Met Tyr
128         115                 120                 125
130 Gly Pro Cys Ala Arg Leu Asn Leu Pro Asn Tyr Arg Ala Ser Glu Glu
131     130                 135                 140
133 Ser Ser Ser Leu Pro Thr Thr Ser Gly Ser Asp Thr Thr Thr Ala Ser
134 145                 150                 155                 160
136 Gly Ile Ser Glu Val Ser Val Tyr Glu Asp Lys Lys Phe Thr Pro Val
137                 165                 170                 175
139 Val Ser Gly Leu Lys Gln Asp Asp Lys Gly Glu Ser Leu Glu Ser Ala
140             180                 185                 190
142 Asp Ser Lys Pro Gln Leu Leu Val Asp Ala Gly Thr Pro Met Ser Ala
143         195                 200                 205
145 Val Lys Glu Glu Pro Lys Glu Tyr Gln Val Met Asp Ser Gln Ser Glu
146     210                 215                 220
148 Gly Gln Phe Gly Asp Glu Glu Pro Pro Ser Lys Leu Val Cys Lys Glu
149 225                 230                 235                 240
151 Val Asp Phe Gly Gln Asp Gln Ala Val Val Pro Ala Val Lys Asn Ala
152                 245                 250                 255
154 Glu Glu Met Gly Gly Glu Met Gly Gly Asp Ile Leu Lys Gly Cys Ser
155             260                 265                 270
157 Leu Ser Glu Met Phe Asp Val Asp Glu Leu Leu Ser Val Leu Asp Ser
158         275                 280                 285
160 Thr Pro Leu His Ala Ser Asp Phe Gln His Gly Met Gly Asn Gly Asn
161     290                 295                 300
163 Val Lys Ala Glu Ala Ala Tyr Asn Tyr Ala Pro Ser Trp Asp Ser Ala
164 305                 310                 315                 320
166 Phe Gln Leu Gln Asn Gln Asp Pro Lys Leu Gly Ser Gln Gln His Met
167                 325                 330                 335
169 Ala Gln Thr Pro Pro Glu Ile Asn Ser Gly Leu Asp Phe Leu Gln Pro
170             340                 345                 350
172 Gly Arg Gln Glu Asp Ser Tyr Phe Thr Leu Gly Asp Leu Asp Phe Leu
173         355                 360                 365
175 Asp Leu Gly Ala Glu Leu Gly Leu
176     370                 375
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 210
182 <212> TYPE: PRT
183 <213> ORGANISM: Catharanthus roseus
185 <400> SEQUENCE: 5
186 Met Tyr Gln Ser Asn Ala His Asn Ser Asp His Leu Thr Phe Leu Pro
187   1               5                  10                  15
189 Pro Leu Val Asp Tyr Gln Phe Leu Asn Asn Asp Phe Asp Phe Ser Glu
190              20                  25                  30
192 Ile Phe Thr Asp Phe Asn Tyr Ala Asn Tyr Asn Tyr Asn Thr Ser Thr
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Input Set : A:\PTO_VSK.txt
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193          35                  40                  45
195 Ser Asp Asn Phe Ser Gly Phe Gln Phe Asn Glu Asn Cys Glu Glu Ile
196      50                  55                  60
198 Ile Ser Pro Asn Tyr Ala Ser Glu Asp Leu Ser Asp Ile Ile Leu Thr
199  65                  70                  75                  80
201 Asp Ile Phe Lys Asp Gln Asp Asn Tyr Glu Asp Glu Val Val Ala Gly
202                  85                  90                  95
204 Glu Gln Glu Glu Glu Leu Ile Thr Thr Pro Thr Ser Arg Gly Gly Gly
205             100                 105                 110
207 Gly Gly Gly Cys Glu Gln Arg Ser Asn Glu Glu Trp Ile Arg Tyr Arg
208         115                 120                 125
210 Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp
211     130                 135                 140
213 Pro Lys Arg Lys Gly Ser Arg Ile Trp Leu Gly Thr Tyr Glu Thr Ala
214 145                 150                 155                 160
216 Glu Asp Ala Ala Leu Ala Phe Asp Gln Ala Ala Phe Gln Leu Arg Gly
217                 165                 170                 175
219 Ser Arg Ala Arg Leu Asn Phe Pro Asn Leu Ile Gly Ser Ala Asn Ala
220             180                 185                 190
222 Pro Val Arg Val Ser Pro Arg Arg Arg Ser Ser Ser Cys His Leu Arg
223         195                 200                 205
225 Pro Gln
226     210
230 <210> SEQ ID NO: 6
231 <211> LENGTH: 203
232 <212> TYPE: PRT
233 <213> ORGANISM: Catharanthus roseus
235 <400> SEQUENCE: 6
236 Met Ser Glu Glu Ile Ile Ser Val Ser Asp Arg Phe Leu Leu Ser Leu
237   1               5                  10                  15
239 Ile Glu Glu His Leu Leu Ser Asp Asn Ser Asp Asp Ser Ser Ser Glu
240              20                  25                  30
242 Leu Thr Ser Thr Glu Glu Asn Trp Glu Glu Ile Phe Ala Asp Phe Leu
243          35                  40                  45
245 Asn Trp Ser Gly Ser Glu Ile Gln Lys Arg Gly Ser Pro Ser Ser Glu
246      50                  55                  60
248 Ser Cys Gln Ser Asn Ser Met Ala Glu Ser Cys Gln Glu Asp Ser Val
249  65                  70                  75                  80
251 Val Gly Thr Pro Pro Glu Ala Ala Ala Gly Gly Gly Cys Ser Lys Asp
252                  85                  90                  95
254 Trp Asn Arg Tyr Lys Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
255             100                 105                 110
257 Ala Glu Ile Arg Asp Pro Lys Lys Lys Gly Ser Arg Ile Trp Leu Gly
258         115                 120                 125
260 Thr Tyr Glu Thr Pro Glu Asp Ala Ala Leu Ala Tyr Asp Ala Ala Ala
261     130                 135                 140
263 Phe Asn Met Arg Gly Ala Lys Ala Arg Leu Asn Phe Pro His Leu Ile
264 145                 150                 155                 160
266 Gly Ser Asn Ile Ser Gly Pro Val Arg Val Asn Pro Arg Lys Arg Phe
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```
267                 165                 170                 175
269 Pro Ala Glu Pro Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser
270             180                 185                 190
272 Glu Asn Ser Gly Gly Arg Lys Lys Arg Arg Tyr
273         195                 200
277 <210> SEQ ID NO: 7
278 <211> LENGTH: 48
279 <212> TYPE: DNA
280 <213> ORGANISM: Catharanthus roseus
282 <400> SEQUENCE: 7
283 gtacatcact cttagaccgc cttctttgaa agtgatttcc cttggacc                48
286 <210> SEQ ID NO: 8
287 <211> LENGTH: 25
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
294 <400> SEQUENCE: 8
295 ccacgtggtt gtagtctctt agacc                                      25
298 <210> SEQ ID NO: 9
299 <211> LENGTH: 25
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
306 <400> SEQUENCE: 9
307 ggtacatcag agaatgaccg ccttc                                      25
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311 <211> LENGTH: 26
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
318 <400> SEQUENCE: 10
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322 <210> SEQ ID NO: 11
323 <211> LENGTH: 21
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
330 <400> SEQUENCE: 11
331 agaccgcgaa gaatgaaagt g                                         21
334 <210> SEQ ID NO: 12
335 <211> LENGTH: 29
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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VERIFICATION SUMMARY DATE: 08/14/2001
PATENT APPLICATION: **US/09/890,782** TIME: 10:55:51

Input Set : **A:\PTO_VSK.txt**
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date